AMENDMENTS

Amendments to the Specification:

Please amend paragraph 0110 of the specification as follows:

[0001] Comparison of sequences and determination of percent identity between two sequences can be accomplished using a mathematical algorithm. Percent identity between two amino acid or nucleotide sequences can be determined using the algorithm of Meyers & Miller, *CABIOS 4:* 11-17 (1989), which has been incorporated into the ALIGN program (version 2.0), using a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4. Also, percent identity between two amino acid sequences can be determined using the Needleman & Wunsch, *J. Mol. Biol. 48:* 444-453 (1970) algorithm which has been incorporated into the GAP program in the GCG software package (available at the ~~http~~ world wide web address ~~www.~~gcg.com), using either a Blossum 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6. Percent identity between two nucleotide sequences can be determined using the GAP program in the GCG software package (available at ~~http~~ world wide web address ~~www.~~gcg.com), using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6. A set of parameters often used is a Blossum 62 scoring matrix with a gap open penalty of 12, a gap extend penalty of 4, and a frameshift gap penalty of 5.

Please amend paragraph 0113 of the specification as follows:

[0002] *ICAM, MAPK10, KIAA0861, NUMA1* or *GALE* nucleotide sequences and *ICAM, MAPK10, KIAA0861, NUMA1* or *GALE* amino acid sequences can be used as "query sequences" to perform a search against public databases to identify other family members or related sequences, for example. Such searches can be performed using the NBLAST and XBLAST programs (version 2.0) of Altschul *et al., J. Mol. Biol. 215:* 403-10 (1990). BLAST nucleotide searches can be performed with the NBLAST program, score =

100, wordlength = 12 to obtain nucleotide sequences homologous to nucleotide sequences from SEQ ID NO: 1-12. BLAST polypeptide searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to polypeptides encoded by a *ICAM, MAPK10, KIAA0861, NUMA1* or *GALE* nucleotide sequence. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al., Nucleic Acids Res. 25(17):* 3389-3402 (1997). When utilizing BLAST and Gapped BLAST programs, default parameters of the respective programs (*e.g.*, XBLAST and NBLAST) can be used (*see* the ~~http~~ world wide web address ~~www.~~ncbi.nlm.nih.gov).

Please amend paragraph 0249 of the specification as follows:

[0003] Table 3 includes information pertaining to the incident polymorphic variant associated with breast cancer identified herein. Public information pertaining to the polymorphism and the genomic sequence that includes the polymorphism are indicated. The genomic sequences identified in Table 3 may be accessed at the ~~http~~ world wide web address ~~www.~~ncbi.nih.gov/entrez/query.fcgi, for example, by using the publicly available SNP reference number (*e.g.*, rs1541998). The chromosome position refers to the position of the SNP within NCBI's Genome Build 33, which may be accessed at the following ~~http~~ world wide web address ~~www.~~ncbi.nlm.nih.gov/mapview/map_search.cgi?chr=hum_chr.inf&query=. The "Contig Position" provided in Table 3 corresponds to a nucleotide position set forth in the contig sequence, and designates the polymorphic site corresponding to the SNP reference number. The sequence containing the polymorphisms also may be referenced by the "Sequence Identification" set forth in Table 3. The "Sequence Identification" corresponds to cDNA sequence that encodes associated target polypeptides (*e.g.*, *NUMA1*) of the invention. The position of the SNP within the cDNA sequence is provided in the "Sequence Position" column of Table 3. Also, the allelic variation at the polymorphic site and the allelic variant identified as associated with breast cancer is specified in Table 3. All nucleotide sequences referenced and accessed by the parameters set forth in Table 3 are

incorporated herein by reference. The positions for these SNPs are indicated in the tables below in Figures 1, 2, 3 and 4, and the incident SNP for the *GALE* region is at position 174 in Figure 5.

Please amend paragraph 0279 of the specification as follows:

[0004] Finally, the gene or genes present in the loci region of the proximal SNPs as annotated by Locus Link (~~http~~ world wide web address ~~www.~~ncbi.nlm.nih.gov/LocusLink/) are provided on the graph. The exons and introns of the genes in the covered region are plotted below each graph at the appropriate chromosomal positions. The gene boundary is indicated by the broken horizontal line. The exon positions are shown as thick, unbroken bars. An arrow is place at the 3' end of each gene to show the direction of transcription.

Please amend paragraph 0281 of the specification as follows:

[0005] Finally, the gene or genes present in the loci region of the proximal SNPs as annotated by Locus Link (~~http~~ world wide web address ~~www.~~ncbi.nlm.nih.gov/LocusLink/) are provided on the graph. The exons and introns of the genes in the covered region are plotted below each graph at the appropriate chromosomal positions. The gene boundary is indicated by the broken horizontal line. The exon positions are shown as thick, unbroken bars. An arrow is place at the 3' end of each gene to show the direction of transcription.

Please amend paragraph 0287 of the specification as follows:

[0006] Finally, the gene or genes present in the loci region of the proximal SNPs as annotated by Locus Link (~~http~~ world wide web address ~~www.~~ncbi.nlm.nih.gov/LocusLink/) are provided on the graph. The exons and introns of the genes in the covered region are plotted below each graph at the appropriate chromosomal positions. The gene boundary is indicated by the broken horizontal line. The exon positions are shown as thick, unbroken bars. An arrow is place at the 3' end of each gene to show the direction of transcription.

Please amend paragraph 0296 of the specification as follows:

[0007] Finally, the gene or genes present in the loci region of the proximal SNPs as annotated by Locus Link (~~http~~ world wide web address ~~www.~~ncbi.nlm.nih.gov/LocusLink/) are provided on the graph. The exons and introns of the genes in the covered region are plotted below each graph at the appropriate chromosomal positions. The gene boundary is indicated by the broken horizontal line. The exon positions are shown as thick, unbroken bars. An arrow is place at the 3' end of each gene to show the direction of transcription.

Please amend paragraph 0307 of the specification as follows:

[0008] RNAi-based gene inhibition was selected as a rapid way to inhibit expression of ICAM1 in cultured cells. siRNA reagents were selectively designed to target the ICAM1 gene. Algorithms useful for designing siRNA molecules specific for ICAM1 gene are disclosed at the ~~http~~ world wide web address ~~www.~~dharmacon.com. siRNA molecules up to 21 nucleotides in length were utilized.